20. The method of claim 19 wherein said complex has the structure

Ligand Component =

fCmGmGrArAfUfCmAmGfUmGmAmAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT (VEGF ligand)

21. The complex of claim 19 wherein said complex is

Ligand Component =

fCmGmGrArAfUfCmAmGfUmGmAmAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT (VEGF ligand)

REMARKS

An Office Action was issued in the above-referenced application on June 8, 1998. All examined claims were rejected. This Amendment and Remarks has been made to respond to such Office Action. Claim 2 is amended and claims 3-21 are added herein. Additional amendments have been made by the Applicants without suggestion by the Examiner, but with the same goal in mind. Any amendments that are made that limit the scope of the claims in any way are done so without prejudice. Claims 3-21 are dependent on either claim 1 or claim 2 and relate to embodiments that are clearly supported in the specification.

Notice to Comply with Sequence Rules

Applicants submitted a response to the Notice to Comply with Requirements for Patent Applications containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures on July 7, 1998.

<u>Informalities</u>

The Examiner has objected to the disclosure because nucleotide sequences in the specification, tables and figures lack SEQ ID NOS. Applicants have added the appropriate SEQ ID NOS to Tables 1-4 and Figures 1A-1E and are submitting substitute tables and figures with this document. Furthermore, the specification has been amended to include SEQ ID NOS where appropriate. Applicants assert that the amendments and the substitute tables and figures do not add any new matter to the application or affect the claimed invention. Withdrawal of this objection is respectfully requested.

Rejections under 35 U.S.C. §112, second paragraph

Claim 2 is rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claim has been amended to specifically address points (a), (b), and (d).

With respect to point (c), the Examiner states that the claim is indefinite in reciting "nucleic acid ligand" which is a general term lacking definition or specificity. Applicants respectfully disagree. Applicants wish to direct the Examiner's attention to page 17, lines 4-26 of the specification where Nucleic Acid Ligand is specifically defined. There is no apparent ambiguity with respect to the definition of this term. As this term has been clearly defined in the specification, withdrawal of this rejection is respectfully requested.

Double Patenting Rejection - Obviousness Type

Claim 1 is provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 5-8 and 11-13 of United States Patent Application No. 08/447,169 (now United States Patent No. 5,811,533) in view of Toole et al. (WO 92/14843). In an effort to expedite prosecution,

Applicants are submitting herewith a Terminal Disclaimer that disclaims the term of the patent issuing on the subject application beyond the term of the aforementioned patent. NeXstar Pharmaceuticals, Inc., is the assignee of record of the entire interest in United States Patent No. 5,811,533. Thus, NeXstar Pharmaceuticals, Inc. is the owner of the subject application and the patent cited by the Examiner. In view of this submission, it is respectfully requested that the provisional obviousness-type double patenting rejection be withdrawn.

Applicants assert that the above-captioned application is in condition for allowance. Prompt consideration of this Amendment and Remarks is earnestly solicited.

This constitutes a request for any needed extension of time and an authorization to charge all fees therefore to Deposit Account No. 22-0277, if not otherwise specifically requested. In addition, the undersigned hereby authorizes the charge of any fee created by the filing of this document to Deposit Account No. 22-0277.

Respectfully submitted,

Date: December 7,1998

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(4)	JC52 :	DIE	Segment
0	H	RADEMA	
	PAT	EMIG	

VEGF165
2
ligands (
-pyrimidine
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		SADEMAN		
Ligand (frequency)		Sequence of variable region 5'-gggaggacgauggggggacgacuggccga-3'	Kd (Ma)	SEQ. ID NO: 10 & 11
Family 1				
VP30.7	<i>₽</i> 0	gAAGAAUUGG UCAUCGUCGCCUCCC	3000	12.
VP30.12	AAUACG	GAAGAAUUGG AUACAUAUGCUCGU	7	13
VP30.13 (7)	GAUAACA	GAAGAAUUGG UGAACAACGUGGU	10	14
VP30.16	AUGAUCGCGUAG	GAAGUAUUGG AAGGCCCU	9	15
VP30.19	CACUUUA	GAAGAAUUGA AUUUCCCGCUGGU	6	91
VP30.22 (6)	UAG	GAAGGAATUGG AAGCGCAUTUUCCUCGY	20	17
VP30.25	CGGGAUUUUG	GAAGAAUUGG AUAUUGGCCU	20	. 81
VP30.26 (2)	CGGYACUUUG	GAAGAAUUGA AUUUCCCGCU	10	19
VP30.27	ъ0	gAAGAAUUGG AUAUAUCGUUCACCCCACCU	400	20
S VP30.40	AAACG	GAAGAAUUGG AUACGCAAGCACGUU	9	21
VP30.41	$\mathbf{U}\mathbf{A}\mathbf{G}$	GAAGUAUUGU AAGCGCCUCGUUUUCGC	7	22
VP30.51 (2)	AGUUUUG	GAAGAAUUGG AUGUUCCGAUCGU	06	23
VP30.54	AAGAAACG	GAAGAAUUGG AGACACGCUCGU	10	24
VP40.4 (5)	5.0	GAAGAAUUGA UGUUGUAUUGUCCUUCCGAUUUCCUGCCGU	200	25
VP40.43	ACA	GAAGAAUUGG GCUUCGCAUUAUCCUCUGUCAGCCGC	30	26
VP40.53	UGAGAGAAACG	GAAGAAUUGG AUACGAUACUCAUCGCGCU	∞	27
VT30.4	CUUAAGUUUUG	GAAGAAUUGA AUACUGGGU	20	28
VT30.7	UAACCAGUG	GAAGAAUUGG CUGCUAUCCU	10	29
VT30.10	AACG	GAAGAAUUGG AUACGUAGCAUGCGU	2	30
VT30.13	CAGGAUUUUG	GAAGAAUUGG AUAUUGGCCGca	10	31
VT30.20	AAACG	GAAGAAUUGG AUACCGCUACGUGUU	4	32
VT30.52	50	gAAGAAUUGA GCAUUCCUUCUUGUGCCU	0006	33
VT30.53 55.0ETV	A AGCUAACG	GAAGAAUUGG AAACAACCGCGUc	10	34

10 Kg/2

Ligand					Sequer	Sequence of variable region	iable re	gion				Kd	SEQ. ID. NO:	.: 0N
(frequency)			5'-888	gaggacg	augcgg [variable re	egion] c	agacgacı	5'-gggaggacgaugcgg [variable region] cagacgacucgcccga-3'			(pM)	10 & 11	,
Family 2											Legentegenstradelista			
VP30.2 (5)	ggYGA	ACCC	ACCGA UGGAA	GAA	מממ	UUGGACGC	၁၅၁	UCGCCU	N.		y	10	35	•
VP30.5 (4)	gAYCA	ACCGA		UUGAC	GUUA	UGGGACGC	၁၅၁	<u>UGGUc</u>	4.14			∞	36.	
VP30.31 (5)	gcggUA	ACCGA		UUGAA	cunc	UUGGACGC	၁၅၁	UACCGU	<u>)(</u>			9	37	•
VP30.43	ggUA	ACCG	ACCGAA UUGAA	GAA	GUUA	UUGGACGC	၁၅၁	UACCU	1			ς	38	٠.
VP40.9	gGAGCAGA	ACCGA		UAGAA	GAA	UUGGACGC	၁၅၁	<u>UCAGC</u>	<u>UCAGCUCC</u> GGGU			30	39	
VP40.14	GUACCAGAA <u>UGAGCA</u> ACCGA	ACCG		AUGAA	GAA	CUGGACGC	၁၅၁	UGCUca	çi			∞	40	
VP40.17	ugcggUGA	ACCGA		UGGAA	UCGC	UUGGACGC	၁၅၁	UCAUC	<u>UCAUCGCA</u> CGUUGCU	ıcu		10	41	
VT30.9 (6)	ggUCA	ACCGG		UUGAA	UAU	nucencec	၁၅၁	<u>UGACC</u> U	ກະ			30	42	
,						٠								
Family 3														
VT30.1 (2)	gacgangegg	A	ACUA		GUGAAUGCUU	SUU AUA	A CGA		ccenennene	N _C		10	43	
VT30.2	<u> </u>		AUCA	GUG	AUCA GUGAAUGCUU	SUU AUA	A GA		<u>ccec</u> cnccen	DS.		7	44	i
VT30.3 (8)	gangegg	AGA	AUCA		GUGAAUGCUU	SUU AUA		AAUC	UCGYGUe			2	45	
VT30.11	gangegg	4	AUCA		GUGAAUGCUU	SUU AUA	A GCUC	<u> </u>	CCGCGUCCU	Ŋ		4	46	٠,
VT30.15	5505	A	ACCA		GUGAAUGCUU	SUU AUA	A AGA	-,	<u>cuac</u> ucau	•		3	47	
VT30.21	cgangcgg		AUCA		GUGAAUGCUU	OU AUA	A GA		<u>CCGUAUUG</u> CGU	cen		9	48	
VT30.28	gangegg	AGA	AUCA		GUGAAUGCUU	SUU AUA		AACC 1	UCGUGUe			09	49	
VT30.29	augcggA		AUCA	ene	AUCA GUGAAUGCUU	SUU AUA	A GC	•	<u>ucceceu</u> geu	au		10	50	•
VT30.35	333		ACCA	909	ACCA GUGAAUGCUU	SUU AUA		AGCCCA 1	<u>UCG</u> ACCU			N.D.	51	
VT30.41	gangcgg	4	CAGG	GUG	CAGG GUGAAUGCCA	CA AUG	- 1	CUUU	UACUUU UCGCGUe	er general de la granda de la companya de la compa	Acceptance and the second of t	40	52	
VT30.44	goggA		AUCA	CUG	AAUGC	WU AU	A CA		AUCA GUGAAUGCUU AUA CA UCCGCUCGGU	3.0° × × 0.00	A. A.	10	53	
VT30.54	<u>Dggog</u>		ACUAC	eng	ACUAG GUGAAUGCCA	CA AUA		UUCUUC 1	<u>UCCGU</u>			10	54	

Table 2. Effect of truncation on high affinity binding of VEGF ligands.

Sequence	Length (nts)	KD (pM)	SEQ ID NO:
			55
	28	3000	56
ACGAUGCGGUAGGAAGAAUUGGAAGCG <u>C</u>	28	80	57
GCGGUAGGAAGAAUUGGAAGCG <u>C</u>	23	90	58
CGGUAGGAAGAAUUGGAAGCG <u>C</u>	22	100	59
GGUAGGAAGAAUUGGAAGCGC*	21	200	60
GUAGGAAGAAUUGGAAGCGC*	20	>100,000	61
GGCGAACCGAUGGAAUUUUUGGACGCUCGCC*	31	20	62
•			63
			64
GAACCGAUGGAAUUUUUGGACGCUC*			65
AACCGAUGGAAUUUUUGGACGCU*	23		66
ACCGAUGGAAUUUUUGGACGC*	21	>100,000	67
GCGGAAUCAGUGAAUGCUUAUACAUCCGC*	29	10	68
			69
			70
			71
			72
			73
	GACGAUGCGGUAGGAAGAAUUGGAAGCGC* GACGAUGCGGUAGGAAGAAUUGGAAGCG ACGAUGCGGUAGGAAGAAUUGGAAGCGC GCGGUAGGAAGAAUUGGAAGCGC CGGUAGGAAGAAUUGGAAGCGC GGUAGGAAGAAUUGGAAGCGC* GUAGGAAGAAUUGGAAGCGC* GGAACCGAUGGAAUUUUUGGACGCUCGCC* GCGAACCGAUGGAAUUUUUGGACGCUCGC CGAACCGAUGGAAUUUUUGGACGCUCG GAACCGAUGGAAUUUUUGGACGCUC* AACCGAUGGAAUUUUUGGACGCUC*	GACGAUGCGGUAGGAAGAAUUGGAAGCGC* GACGAUGCGGUAGGAAGAAUUGGAAGCGC ACGAUGCGGUAGGAAGAAUUGGAAGCGC ACGAUGCGGUAGGAAGAAUUGGAAGCGC CGGUAGGAAGAAUUGGAAGCGC CGGUAGGAAGAAUUGGAAGCGC CGGUAGGAAGAAUUGGAAGCGC CCGGUAGGAAGAAUUGGAAGCGC CCGGUAGGAAGAAUUGGAAGCGC CCGGUAGGAAGAAUUGGAAGCGC* CGGAAGGAAGAAUUGGAAGCGC* CGGAACCGAUGGAAUUUUUGGACGCUCGCC CGAACCGAUGGAAUUUUUGGACGCUCGC CGAACCGAUGGAAUUUUUGGACGCUCGC CGAACCGAUGGAAUUUUUGGACGCUCC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAACCGAUGGAAUUUUUGGACGCUC* CGAAUCAGUGAAUGCUUAUACAUCCGC* CGGAAUCAGUGAAUGCUUAUACAUCCGC* CGGAAUCAGUGAAUGCUUAUACAUCCC CCGGAAUCAGUGAAUGCUUAUACAUCCC CCGGAAUCAGUGAAUGCUUAUACAUCCC CCGGAAUCAGUGAAUGCUUAUACAUCCC CCGGAAUCAGUGAAUGCUUAUACAUCCC CCGGAAUCAGUGAAUGCUUAUACAUCCC CCGAAUCAGUGAAUGCUUAUACAUCCC CCGGAAUCAGUGAAUGCUUAUACAUCCC CCGAAUCAGUGAAUGCUUAUACAUCCC	GACGAUGCGGUAGGAAGAAUUGGAAGCGC* 29 70 GACGAUGCGGUAGGAAGAAUUGGAAGCG 28 3000 ACGAUGCGGUAGGAAGAAUUGGAAGCGC 28 80 GCGGUAGGAAGAAUUGGAAGCGC 28 90 CGGUAGGAAGAAUUGGAAGCGC 23 90 CGGUAGGAAGAAUUGGAAGCGC 22 100 GGUAGGAAGAAUUGGAAGCGC 22 100 GUAGGAAGAAUUGGAAGCGC* 21 200 GUAGGAAGAAUUGGAAGCGC* 21 200 GUAGGAAGAAUUGGAAGCGC* 20 >100,000 GGCGAACCGAUGGAAUUUUUGGACGCUCGCC* 31 20 CGAACCGAUGGAAUUUUUGGACGCUCGC 29 40 CGAACCGAUGGAAUUUUUGGACGCUCGC 27 100 GAACCGAUGGAAUUUUUGGACGCUC* 25 200 AACCGAUGGAAUUUUUGGACGCUC* 21 >100,000 GCGGAAUCAGUGAAUGCUUAUACAUCCGC* 29 10 CGGAAUCAGUGAAUGCUUAUACAUCCGC* 29 10 GGAAUCAGUGAAUGCUUAUACAUCCGC* 29 10 GGAAUCAGUGAAUGCUUAUACAUCCGC* 29 10 GGAAUCAGUGAAUGCUUAUACAUCCGC* 29 10 GGAAUCAGUGAAUGCUUAUACAUCCG 27 10 GGAAUCAGUGAAUGCUUAUACAUCCG 25 60 GAAUCAGUGAAUGCUUAUACAUCC* 23 2000 AAUCAGUGAAUGCUUAUACAUCC* 23 2000 AAUCAGUGAAUGCUUAUACAUC* 23 2000



Table 3. Effect of 2'-OMe-purine substitutions on affinity for VEGF.

1) F)

Ligand	Sequence	K _D (pM)	SEQ NO:
t22OMe (OH-10,12,22)	GACGAUGCG <u>G</u> U <u>A</u> GGAAGAAUU <u>G</u> GAAGCGC	10	74
t22OMe (OH-10,12)	GACGAUGCG <u>G</u> U <u>A</u> GGAAGAAUUGGAAGCGC	20	75
t22OMe (OH-10,22)	GACGAUGCGGUAGGAAGAAUUGGAAGCGC	4,000	76
t22OMe (OH-12,22)	GACGAUGCGGU <u>A</u> GGAAGAAUU <u>G</u> GAAGCGC	90	77
t2OMe (OH-6,21)	GGCGAACCGAUGGAAUUUUUGGACGCUCGCC	60	78
t2OMe (OH-6)	GGCGAACCGAUGGAAUUUUUUGGACGCUCGCC	500	79
t2OMe (OH-21)	GGCGAACCGAUGGAAUUUUUUGGACGCUCGCC	20,000	80
t44OMe (OH-5,6)	GCGG <u>AA</u> UCAGUGAAUGCUUAUACAUCCGC	40	81
t44OMe (OH-5)	GCGGAAUCAGUGAAUGCUUAUACAUCCGC	>100,000	82
t44OMe (OH-6)	GCGGAAUCAGUGAAUGCUUAUACAUCCGC	>100,000	83

Table 4. Binding Parameters of 2'-Ome-substituted minimal ligands.

Ligand	Sequence	K _D (s.d.) (pM)	k _d (s.d.) (sec ⁻¹)	k_a SEQ $(M^{-1}sec^{-1})$ ID NO:	SEQ ID NO:
t220Me	GCGGUAGGAAGAAUUGGAAGCGC	67 (36)	0.012 (0.004)	1.8×10^{8}	84
t20Me	t20Me GCGAACCGAUGGAAUUUUUGGACGCUCGC 140 (50)	140 (50)	0.0042 (0.002)	3.0×10^{7}	85
t440Me	440Me CGGAAUCAGUGAAUGCUUAUACAUCCG	51 (11)	0.0074 (0.002)	1.5×10^{8}	98

NX31838 - PL

fCmGmGrArAfUfCmAmGfUmGmAmAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT

(VEGF ligand)

Ligand Component =

SEQ. ID NO.: 5

FIGURE 1A

NX31838 Lipid-amide 1

fCmGmGrArAfUfCmAmGfUmGmAmAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT

(VEGF ligand)

Ligand Component =

SEQ. ID NO.:6

FIGURE 1B

After 3.25 ep

$$C_{17}H_{35}$$
 $C_{17}H_{35}$
 $C_{17}H_{35}$

NX31838 Lipid-amide 2

Ligand Component =

fCmGmGrArAfUfCmAmGfUmGmAmAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT (VEGF ligand)

NX31838 40K mPEG

fCmGmGrArAfUfCmAmGfUmGmAmAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT Ligand Component = (VEGF ligand)

FIGURE 1D SEQ. ID NO.: 8

NX31838 20Km PEG

Ligand Component = fCmGmGramAfUmGfCfUfUmAfUmAfCmAfUfCfCmG-3'3'-dT (VEGF ligand)

FIGURE 1E SEQ. ID NO.: 9